

**Remarks**

Claims 116, 124-131 and 139-144 are presently pending in the subject application. Claims 131 and 139-144 were previously withdrawn. Reconsideration and allowance in view of the above amendments and the following remarks are hereby respectfully requested.

**Rejection Under 35 U.S.C. § 102**

Claims 116 and 124-130 stand rejected by the Examiner under 35 U.S.C. § 102(e) as being anticipated by Peiris *et al.* (U.S. Patent Application Publication No. US 2005/0009009 A1). Applicants respectfully traverse this rejection for the reasons that follow.

This rejection is maintained on the ground that the terms “its complement” and “DNA equivalents” are broad terms that are not defined by the specification. This is not so. These terms have the following specific meanings provided in the Definitions section of the application.

By “complement” is meant, unless otherwise indicated, a sequence which is the perfect complement of the referred sequence (*i.e.*, the “complement” is of the same length as and the perfect complement of the referred sequence). *See* specification at page 21, lines 1-3.

By “RNA and DNA equivalents” or “RNA and DNA equivalent bases” is meant RNA and DNA molecules having the same complementary base pair hybridization properties. RNA and DNA equivalents have different sugar moieties (*i.e.*, ribose versus deoxyribose) and may differ by the presence of uracil in RNA and thymine in DNA. The differences between RNA and DNA equivalents do not contribute to differences in homology because the equivalents have the same degree of complementarity to a particular sequence. *See* specification at page 25, lines 22-27.

Based on these definitions of the recited terms, it is clear that the claims cannot encompass sequences that share as few as one complementary nucleotide or one DNA equivalent nucleotide. The Examiner has suggested amending claim 116 to recite “the complement of SEQ ID NO:3.”

While Applicants view this as a semantical difference, the suggested change has nevertheless been made to claim 116. Additionally, Applicants have amended claim 116 to recite “the DNA equivalent of SEQ ID NO:3” and “the DNA equivalent of the complement of SEQ ID NO:3.” The new claim language is identical in scope to the previous wording of the claims. Accordingly, for the reasons presented, withdrawal of this rejection is hereby respectfully requested.

**Rejection Under 35 U.S.C. § 103**

Claims 116 and 124-130 stand rejected by the Examiner under 35 U.S.C. § 103(a) as being unpatentable over GenBank Accession No. NC\_004718.1 in view of Peiris *et al.* (U.S. Patent Application Publication No. US 2005-0009009 A1). GenBank Accession No. NC\_004718.1 is cited for disclosing the complete genomic sequence of the SARS coronavirus, and Peiris is cited for teaching the use of oligonucleotides in a diagnostic assay for detecting SARS. Applicants respectfully traverse this rejection for the reasons that follow.

To the extent that this rejection is being maintained on the ground that the terms “its complement” and “DNA equivalents” are overly broad, Applicants submit that this rejection is improper for the reasons set forth in their response to the Section 102 rejection above.

Additionally, Applicants previously pointed out that other detection probes were designed and tested that overlapped with but were not contained within the target binding portion of the claimed probes. The sequences of these probes are identified by SEQ ID Nos. 44 and 45. The target binding portion of SEQ ID NO:44 shares six contiguous bases in common with the 5'-end of SEQ ID NO:3, and the target binding portion of SEQ ID NO:45 shares six contiguous bases in common with the 3'-end of SEQ ID NO:3 (Applicants mistakenly indicated that there was only a five base overlap for each of these probes in their prior response). While the specification states that it is *possible* that these probes could be optimized to detect target amplicon, optimization would involve changing the probe sequences, most logically by tiling toward a sequence shown to exhibit the

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desired hybridization characteristics (*i.e.*, a sequence contained within SEQ ID NO:3) and gathering empirical data to determine their usefulness. Thus, it has been shown that the overlapping probes do not perform as well as the claimed probes, and the usefulness of modified forms of these overlapping probes could not be determined without further experimentation. Thus, Applicants maintain that the claimed probes have superior detection properties that could not be predicted.

For the reasons presented, Applicants submit that the claims are fully patentable in view of the cited art. Accordingly, withdrawal of this rejection is hereby respectfully requested.

**Conclusion**

Applicants submit that the subject application is in condition for allowance and, accordingly, early notice to that effect is respectfully requested.

Please charge fees due in connection with this Request to Deposit Account No. 07-0835 in the name of Gen-Probe Incorporated. No fees are believed to be due.

Respectfully submitted,

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